

SEQUENCE LISTING

<110> Wang, Danher

<120> GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS

<130> 22488-712

<150> 09/585,599

<151> 2000-06-02

<150> PCT/US01/18238

<151> 2001-06-04

<160> 75

<170> PatentIn version 3.1

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<213> Ebola virus

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10003035-110101

10003035-110101

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<212> DNA

<213> Artificial sequence

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<223> Modified Env

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 <212> DNA
 <213> Artificial sequence

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 <223> Full length Gag

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 <213> Human immunodeficiency virus type 1

<400> 18

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His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Leu Gln Pro Ser Leu
 35 40 45

Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr
 50 55 60

Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp Thr Lys Glu Ala
 65 70 75 80

Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys Lys Lys Ala Gln
 85 90 95

Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val Ser Gln Asn Tyr
 100 105 110

Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His Gln Ala Ile Ser
115 120 125

Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu Lys Ala Phe
130 135 140

Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala Thr
145 150 155 160

Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln Ala
165 170 175

Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu Trp
180 185 190

Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln Met
195 200 205

Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln
210 215 220

Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly Glu
225 230 235 240

Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg Met
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Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro
260 265 270

Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln
275 280 285

Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val Gln
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Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala
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Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly Pro
325 330 335

Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Val Thr Asn
340 345 350

10003035-110101

Thr Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg Asn Gln Arg Lys
355 360 365

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370 375 380

Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly
385 390 395 400

His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys
405 410 415

Ile Trp Pro Ser Tyr Lys Gly Arg Pro Gly Asn Phe Leu Gln Ser Arg
420 425 430

Pro Glu Pro Thr Ala Pro Pro Phe Leu Gln Ser Arg Pro Glu Pro Thr
435 440 445

Ala Pro Pro Glu Glu Ser Phe Arg Ser Gly Val Glu Thr Thr Thr Pro
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Leu Arg Ser Leu Phe Gly Asn Asp Pro Ser Ser Gln
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<220>
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<220>
<223> Modified Env/Nef from strain BH10

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 <212> DNA
 <213> Artificial sequence

<220>
 <223> Modified Env/Tat from strain BH10

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aaaacaataa	tctttaagca	gtcctcagga	ggggaccag	aaattgtaac	gcacagtttt	1140
aattgtggag	gggaattttt	ctactgtaat	tcaacacaac	tgtttaatag	tacttggttt	1200
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ccatgcagaa	taaaacaaat	tataaacatg	tggcaggaag	taggaaaagc	aatgtatgcc	1320
cctcccatca	gtggacaaat	tagatgttca	tcaaataatta	cagggctgct	attaacaaga	1380
gatggtggta	atagcaacaa	tgagtccgag	atcttcagac	ctggaggagg	agatatgagg	1440
gacaattgga	gaagtgaatt	atataaatat	aaagtagtaa	aaattgaacc	attaggagta	1500
gcaccaccca	aggcaaagag	aagagtgggtg	cagagagaaa	aaagagcagt	gggaatagga	1560
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ctgacggtac	aggccagaca	attattgtct	ggtatagtgc	agcagcagaa	caatttgctg	1680
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ggttgctctg	gaaaactcat	ttgcaccact	gctgtgcctt	ggaatgctag	ttggagtaat	1860
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gaacaagaat	tattggaatt	agataaatgg	gcaagtttgt	ggaattgggt	taacataaca	2040
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tttcagaccc	acctccaat	cccgagggga	cccagacaggc	ccgaaggaat	agaagaagaa	2220
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tgggacgata	tgcggagcct	gtgcctcttc	agctaccacc	gcttgagaga	cttactcttg	2340

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 tggaatctcc tacagtattg gagtcaggag ctaaagaata gtgctgttag cttgtcfaat 2460
 gccacagcta tagcagtagc tgaggggaca gataggggta tagaagtagt acaaggagct 2520
 tatagagcta ttcgccacat acctagaaga ataagacagg gcttggaaag gattttgcta 2580
 taa 2583

<210> 25
 <211> 108
 <212> DNA
 <213> Human immunodeficiency virus type 1

<400> 25
 tgtacaagac ccaacaacaa tacaagaaaa agtatccgta tccagagagg accagggaga 60
 gcatttggtta caataggaaa aataggaaat atgagacaag cacattgt 108

<210> 26
 <211> 105
 <212> DNA
 <213> Human immunodeficiency virus type 1

<400> 26
 tgtaccagac ctaacaacaa tacaagaaaa agtgtacgta taggaccagg acaaacattc 60
 tatgcaacag gtgatataat aggggatata agacaagcac attgt 105

<210> 27
 <211> 105
 <212> DNA
 <213> Human immunodeficiency virus type 1

<400> 27
 tgtacgagac ccaacaataa tacaagaaaa agtataagga taggaccagg acaagcattc 60
 tatgcaacag gagaaataat aggagatata agacaagcac attgt 105

<210> 28
 <211> 102
 <212> DNA
 <213> Human immunodeficiency virus type 1

<400> 28
 tgcacaaggc cctacaacaa tataagacaa aggaccccca taggactagg gcaagcactc 60
 tataacaacaa gaagaataga agatataaga agagcacatt gt 102

<210> 29
 <211> 105
 <212> DNA
 <213> Human immunodeficiency virus type 1

10003035-110101

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<400> 29
tgtaccagac cctccaccaa tacaagaaca agtatacgta taggaccagg acaagtattc 60

tatagaacag gagacataac aggagatata agaaaagcat attgt 105

<210> 30
<211> 105
<212> DNA
<213> Human immunodeficiency virus type 1

<400> 30
tgtacaagac ccaacaacaa tacaagaaaa agaatatctt taggaccagg acgagtattt 60

tatacagcag gagaaataat aggagacatc agaaaggcac attgt 105

<210> 31
<211> 105
<212> DNA
<213> Human immunodeficiency virus type 1

<400> 31
tgtaccagac ctaataacaa tacaagaaaa agtataactt ttgcaccagg acaagcgctc 60

tatgcaacag gtgaaataat aggagatata agacaagcac attgt 105

<210> 32
<211> 2562
<212> DNA
<213> Artificial sequence

<220>
<223> Env with multi-clade V3 loops

<400> 32
atgagagtga aggagaaata tcagcacttg tggagatggg ggtggagatg gggcaccatg 60

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ggggtacctg tgtggaagga agcaaccacc actctatttt gtgcatcaga tgctaaagca 180

tatgatacag aggtacataa tgtttgggcc acacatgcct gtgtaccac agacccaac 240

ccacaagaag tagtattggt aaatgtgaca gaaaatttta acatgtggaa aaatgacatg 300

gtagaacaga tgcattgagga tataatcagt ttatgggatc aaagcctaaa gccatgtgta 360

aaattaaccc cactctgtgt tggagctggt agttgtaaca cctcagtcac tacacaggcc 420

tgtccaaagg taccctttga gccaatccc atacattatt gtgccccggc tggttttgcg 480

attctaaaat gtaataataa gacgttcaat ggaacaggac catgtacaaa tgtcagcaca 540

gtacaatgta cacatggaat taggccagta gtatcaactc aactgctggt aaatggcagt 600

ctggcagaag aagaggtagt aattagatct gccaatcca cagacaatgc taaaaccata 660

atagtacagc tgaaccaatc tgtagaaatt aattgtacaa gacccaacaa caatacaga 720

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aaaagtatcc gtatccagag aggaccaggg agagcatttg ttacaatagg aaaaatagga	780
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gtacgtatag gaccaggaca aacattctat gcaacaggtg atataatagg ggatataaga	900
caagcacatt gttgtacgag acccaacaat aatacaagaa aaagtataag gataggacca	960
ggacaagcat tctatgcaac aggagaaata ataggagata taagacaagc acattgttgc	1020
acaaggccct acaacaatat aagacaaagg acccccatag gactagggca agcactctat	1080
acaacaagaa gaatagaaga tataagaaga gcacattggt gtaccagacc ctccaccaat	1140
acaagaacaa gtatacgtat aggaccagga caagtattct atagaacagg agacataaca	1200
ggagatataa gaaaagcata ttgtggatcc tgtacaagac ccaacaacaa tacaagaaaa	1260
agaatatctt taggaccagg acgagtattt tatacagcag gagaaataat aggagacatc	1320
agaaaggcac attgttgtac cagacctaat aacaatacaa gaaaaagtat aacttttgca	1380
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agagaacaat ttggaaataa taaaacaata atctttaagc agtcctcagg aggggaccca	1560
gaaattgtaa cgcacagttt taattgtgga ggggaatttt tctactgtaa ttcaacacaa	1620
ctgtttaata gtacttggtt taatagtact tggagtacta aagggtcaaa taacactgaa	1680
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gtaggaaaag caatgtatgc cctcccatc agtggacaaa ttagatgttc atcaaatatt	1800
acagggtgac tattaacaag agatggtggt aatagcaaca atgagtccga gatcttcaga	1860
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aaaattgaac cattaggagt agcaccacc aaggcaaaga gaagagtggg gcagactagt	1980
gcagtgggaa taggagcttt gtcccttggg ttcttgggag cagcaggaag cactatgggc	2040
gcagcgtcaa tgacgtgac ggtacaggcc agacaattat tgtctggtat agtgcagcag	2100
cagaacaatt tgctgagggc tattgaggcg caacagcatc tgttgcaact cacagtctgg	2160
ggcatcaagc agctccaggc aagaatcctg gctgtggaaa gatacctaaa ggatcaacag	2220
ctcctgggga tttgggggtt ctctggaaaa ctcatctgca ccaactgctgt gccttggaat	2280
gctagttgga gtaataaatc tctggaacag atttggaata acatgacctg gatggagtgg	2340
gacagagaaa ttaacaatta cacaagctta atacactcct taattgaaga atcgcaaaac	2400
cagcaagaaa agaattgaaca agaattattg gaattagata aatgggcaag tttgtggaat	2460
tggtttaaca taacaaattg gctgtggtat ataaaatcgt ggctgctgct gctcctgctc	2520
tcctctccc tcctccaggc caggatttc atgtccctgt ga	2562

<210> 33
 <211> 853
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Modified Env with multi-clade V3 loops

<400> 33

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
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Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
 20 25 30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
 35 40 45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
 50 55 60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
 65 70 75 80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
 85 90 95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
 100 105 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Gly
 115 120 125

Ala Gly Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
 130 135 140

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
 145 150 155 160

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
 165 170 175

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
 180 185 190

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile

10003035-110101

10003035-110101

195					200					205					
Arg	Ser	Ala	Asn	Phe	Thr	Asp	Asn	Ala	Lys	Thr	Ile	Ile	Val	Gln	Leu
210						215					220				
Asn	Gln	Ser	Val	Glu	Ile	Asn	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg
225					230					235					240
Lys	Ser	Ile	Arg	Ile	Gln	Arg	Gly	Pro	Gly	Arg	Ala	Phe	Val	Thr	Ile
				245					250					255	
Gly	Lys	Ile	Gly	Asn	Met	Arg	Gln	Ala	His	Cys	Leu	Gly	Cys	Thr	Arg
			260					265					270		
Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Val	Arg	Ile	Gly	Pro	Gly	Gln	Thr
			275					280				285			
Phe	Tyr	Ala	Thr	Gly	Asp	Ile	Ile	Gly	Asp	Ile	Arg	Gln	Ala	His	Cys
	290					295					300				
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	Arg	Ile	Gly	Pro
305					310					315					320
Gly	Gln	Ala	Phe	Tyr	Ala	Thr	Gly	Glu	Ile	Ile	Gly	Asp	Ile	Arg	Gln
				325					330					335	
Ala	His	Cys	Cys	Thr	Arg	Pro	Tyr	Asn	Asn	Ile	Arg	Gln	Arg	Thr	Pro
			340					345					350		
Ile	Gly	Leu	Gly	Gln	Ala	Leu	Tyr	Thr	Thr	Arg	Arg	Ile	Glu	Asp	Ile
		355					360					365			
Arg	Arg	Ala	His	Cys	Cys	Thr	Arg	Pro	Ser	Thr	Asn	Thr	Arg	Thr	Ser
	370					375					380				
Ile	Arg	Ile	Gly	Pro	Gly	Gln	Val	Phe	Tyr	Arg	Thr	Gly	Asp	Ile	Thr
385					390				395						400
Gly	Asp	Ile	Arg	Lys	Ala	Tyr	Cys	Gly	Ser	Cys	Thr	Arg	Pro	Asn	Asn
				405					410					415	
Asn	Thr	Arg	Lys	Arg	Ile	Ser	Leu	Gly	Pro	Gly	Arg	Val	Phe	Tyr	Thr
			420					425					430		
Ala	Gly	Glu	Ile	Ile	Gly	Asp	Ile	Arg	Lys	Ala	His	Cys	Cys	Thr	Arg
		435					440					445			

Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Phe Ala Pro Gly Gln Ala
450 455 460

Leu Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys
465 470 475 480

Leu Gly Asn Ile Ser Arg Ala Lys Trp Asn Asn Thr Leu Lys Gln Ile
485 490 495

Asp Ser Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe
500 505 510

Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn
515 520 525

Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser
530 535 540

Thr Trp Phe Asn Ser Thr Trp Ser Thr Lys Gly Ser Asn Asn Thr Glu
545 550 555 560

Gly Ser Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn
565 570 575

Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly
580 585 590

Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp
595 600 605

Gly Gly Asn Ser Asn Asn Glu Ser Glu Ile Phe Arg Pro Gly Gly Gly
610 615 620

Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val
625 630 635 640

Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val
645 650 655

Val Gln Thr Ser Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
660 665 670

Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val
675 680 685

10003035-110101

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
690 695 700

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
705 710 715 720

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Leu
725 730 735

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
740 745 750

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
755 760 765

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
770 775 780

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
785 790 795 800

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
805 810 815

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
820 825 830

Ser Trp Leu Leu Leu Leu Leu Leu Ser Leu Ser Leu Leu Gln Ala Thr
835 840 845

Asp Phe Met Ser Leu
850

<210> 34
<211> 1092
<212> DNA
<213> Human immunodeficiency virus type 1

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ctagaacgat tcgcagttaa tcctggcctg ttagaaacat cagaaggctg tagacaaata 180
ctgggacagc tacaaccatc ccttcagaca ggatcagaag aacttagatc attatataat 240
acagtagcaa ccctctattg tgtgcatcaa aggatagaga taaaagacac caaggaagct 300

ttagacaaga tagaggaaga gcaaaacaaa agtaagaaaa aagcacagca agcagcagct	360
gacacaggac acagcagtca ggtcagccaa aattacccta tagtgcagaa catccagggg	420
caaatggtac atcaggccat atcacctaga actttaaatg catgggtaaa agtagtagaa	480
gagaaggctt tcagcccaga agtaataccc atgttttcag cattatcaga aggagccacc	540
ccacaagatt taaacaccat gctaaacaca gtgggggggac atcaagcagc catgcaaatg	600
ttaaaagaga ccatcaatga ggaagctgca gaatgggata gagtacatcc agtgcattgca	660
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agtacccttc aggaacaaat aggatggatg acaaataatc cacctatccc agtaggagaa	780
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tataaaactc taagagccga gcaagcttca caggaggtaa aaaattggat gacagaaacc	960
ttgttggtcc aaaatgcgaa cccagattgt aagactatct taaaagcatt gggaccagcg	1020
gctacactag aagaaatgat gacagcatgt caggagtag gaggaccgg ccataaggca	1080
agagttttgt aa	1092

<210> 35
 <211> 1179
 <212> DNA
 <213> Human immunodeficiency virus type 1

<400> 35	
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gaattagatc gatgggaaaa aattcgggta aggccagggg gaaagaaaaa atataaatta	180
aaacatatag tatgggcaag caggagctga gaacgattcg cagttaatcc tggcctgtta	240
gaaacatcag aaggctgtag acaaatactg ggacagctac aaccatccct tcagacagga	300
tcagaagaac ttagatcatt atataataga gtagcaacct tctatttgtg gcatcaaagg	360
atagagataa aagacaccaa ggaagcttta gacaagatag aggaagagca aaacaaaagt	420
aagaaaaaag cacagcaagc agcagctgac acaggacaca gcagtcaggt cagccaaaat	480
tacctatag tgcagaacat ccaggggcaa atggtacatc aggccatata acctagaact	540
ttaatgcat gggtaaaagt agtagaagag aaggctttca gccagaagt aatacccatg	600
ttttcagcat tatcagaagg agccacccca caagatttaa acaccatgct aaacacagtg	660
gggggacatc aagcagccat gcaaatgtta aaagagacca tcaatgagga agctgcagaa	720
tgggatagag tacatccagt gcatgcaggg cctattgcac caggccagat gagagaacca	780

10030305.110101

195	200	205
Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala		
210	215	220
Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr		
225	230	235 240
Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile		
	245	250 255
Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys		
	260	265 270
Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly		
	275	280 285
Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu		
	290	295 300
Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr		
305	310	315 320
Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala		
	325	330 335
Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly		
	340	345 350
Val Gly Gly Pro Gly His Lys Ala Arg Val Leu		
	355	360
<210> 38		
<211> 410		
<212> PRT		
<213> Human immunodeficiency virus type 1		
<400> 38		
Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg		
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	20	25 30
Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp Glu Lys Ile		
	35	40 45

Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys His Ile Val
50 55 60

Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro Gly Leu Leu
65 70 75 80

Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu Gln Pro Ser
85 90 95

Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn Thr Val Ala
100 105 110

Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp Thr Lys Glu
115 120 125

Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys Lys Lys Ala
130 135 140

Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val Ser Gln Asn
145 150 155 160

Tyr Pro Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val Ser
165 170 175

Gln Asn Tyr Pro Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln
180 185 190

Val Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val
195 200 205

His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val
210 215 220

Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu
225 230 235 240

Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val
245 250 255

Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu
260 265 270

Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile
275 280 285

10003035-110101

Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr
290 295 300

Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro
305 310 315 320

Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn
325 330 335

Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln
340 345 350

Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr
355 360 365

Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Thr Ile Leu Lys Ala Leu
370 375 380

Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val
385 390 395 400

Gly Gly Pro Gly His Lys Ala Arg Val Leu
405 410

<210> 39
<211> 453
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 39

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Gly Ala
20 25 30

Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp Glu Lys Ile
35 40 45

Arg Leu Arg Pro Gly Gly Leu Ser Gly Gly Glu Leu Asp Arg Trp Glu
50 55 60

Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys His
65 70 75 80

Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro Gly
85 90 95

10003035.110101

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aaacatatag	tatgggcaag	cagggagcta	gaacgattcg	cagttaatcc	tggcctgtta	240
gaaacatcag	aaggctgtag	acaaatactg	ggacagctac	aaccatccct	tcagacagga	300
tcagaagaac	ttagatcatt	atataataca	gtagcaaccc	tctattgtgt	gcatcaaagg	360
atagagataa	aagacaccaa	ggaagcttta	gacaagatag	aggaagagca	aaacaaaagt	420
aagaaaaaag	cacagcaagc	agcagctgac	acaggacaca	gcagtcaggt	cagccaaaat	480
tactaa						486

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<210> 42
<211> 615
<212> DNA
<213> Human immunodeficiency virus type 1
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[illegible]

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<210> 43
<211> 132
<212> PRT
<213> Human immunodeficiency virus type 1
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<400> 43

Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp
1 5 10 15

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
20 25 30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
50 55 60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
85 90 95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
100 105 110

Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val
115 120 125

Ser Gln Asn Tyr
130

<210> 44
<211> 179
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 44

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Gly Ala
20 25 30

Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp Glu Lys Ile
35 40 45

Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys His Ile Val
50 55 60

Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro Gly Leu Leu
65 70 75 80

Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu Gln Pro Ser
85 90 95

Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Gly Gln Leu Gln

10003035-110101

10003035-110101

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100                                105                                110

Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn Thr
115                                120                                125

Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp Thr
130                                135                                140

Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys Lys
145                                150                                155                                160

Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val Ser
165                                170                                175

Gln Asn Tyr

<210> 45
<211> 186
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 45

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Gly Ala
20 25 30

Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp Glu Lys Ile
35 40 45

Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys His Ile Val
50 55 60

Trp Ala Ser Arg Glu Leu Glu Arg Gly Gln Leu Gln Pro Ser Leu Gln
65 70 75 80

Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr Leu
85 90 95

Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp Thr Lys Glu Ala Leu
100 105 110

Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys Lys Lys Ala Gln Gln
115 120 125
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Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val Ser Gln Asn Tyr Leu
130 135 140

Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala
145 150 155 160

Val Leu Ser Val Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser
165 170 175

Phe Gln Thr His Leu Pro Ile Pro Arg Gly
180 185

<210> 46
<211> 699
<212> DNA
<213> Human immunodeficiency virus type 1

<400> 46
atgcctatag tgcagaacat ccaggggcaa atggtacatc aggccatatc acctagaact 60
ttaaattgcat gggtaaaagt agtagaagag aaggctttca gcccagaagt aatacccatg 120
ttttcagcat tatcagaagg agccacccca caagatttaa acaccatgct aaacacagtg 180
gggggacatc aagcagccat gcaaattgta aaagagacca tcaatgagga agctgcagaa 240
tgggatagag tacatccagt gcatgcaggg cctattgcac caggccagat gagagaacca 300
aggggaagtg acatagcagg aactactagt acccttcagg aacaaatagg atggatgaca 360
aataatccac ctatcccagt aggagaaatt tataaaagat ggataatcct gggattaaat 420
aaaatagtaa gaatgtatag ccctaccagc attctggaca taagacaagg accaaaagaa 480
ccttttagag actatgtaga ccggttctat aaaactctaa gagccgagca agcttcacag 540
gaggtaaaaa attggatgac agaaaccttg ttggtccaaa atgcgaaccc agattgtaag 600
actatttttaa aagcattggg accagcggct aactagaag aaatgatgac agcatgtcag 660
ggagtaggag gacccgcca taaggcaaga gttttgtaa 699

<210> 47
<211> 786
<212> DNA
<213> Human immunodeficiency virus type 1

<400> 47
atgagagtga aggagaaata tcagcacttg tggagatggg ggtggagatg gggcaccatg 60
ctccttggga tggtgatgat ctgtagtgtc cctatagtgc agaacatcca ggggcaaagt 120
gtacatcagg ccatatcacc tagaacttta aatgcatggg taaaagtagt agaagagaag 180
gctttcagcc cagaagtaat acccatgttt tcagcattat cagaaggagc caccacacaa 240

gatttaaaca ccatgctaaa cacagtgggg ggacatcaag cagccatgca aatgttaaaa 300
gagaccatca atgaggaagc tgcagaatgg gatagagtac atccagtgca tgcagggcct 360
attgcaccag gccagatgag agaaccaagg ggaagtgaca tagcaggaac tactagtacc 420
cttcaggaac aaataggatg gatgacaaat aatccaccta tcccagtagg agaaatttat 480
aaaagatgga taatcctggg attaaataaa atagtaagaa tgtatagccc taccagcatt 540
ctggacataa gacaaggacc aaaagaacct tttagagact atgtagaccg gttctataaa 600
actctaagag ccgagcaagc ttcacaggag gtaaaaaatt ggatgacaga aaccttggtg 660
gtccaaaatg cgaaccaga ttgtaagact attttaaaag cattgggacc agcggctaca 720
ctagaagaaa tgatgacagc atgtcagggg gtaggaggac ccggccataa ggcaagagtt 780
ttgtaa 786

<210> 48
<211> 915
<212> DNA
<213> Human immunodeficiency virus type 1

<400> 48
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ctccttggga tggtgatgat ctgtagtgt cctatagtgc agaacatcca ggggcaaagt 120
gtacatcagg ccatatcacc tagaacttta aatgcatggg taaaagtagt agaagagaag 180
gctttcagcc cagaagtaat acccatgttt tcagcattat cagaaggagc caccacacaa 240
gatttaaaca ccatgctaaa cacagtgggg ggacatcaag cagccatgca aatgttaaaa 300
gagaccatca atgaggaagc tgcagaatgg gatagagtac atccagtgca tgcagggcct 360
attgcaccag gccagatgag agaaccaagg ggaagtgaca tagcaggaac tactagtacc 420
cttcaggaac aaataggatg gatgacaaat aatccaccta tcccagtagg agaaatttat 480
aaaagatgga taatcctggg attaaataaa atagtaagaa tgtatagccc taccagcatt 540
ctggacataa gacaaggacc aaaagaacct tttagagact atgtagaccg gttctataaa 600
actctaagag ccgagcaagc ttcacaggag gtaaaaaatt ggatgacaga aaccttggtg 660
gtccaaaatg cgaaccaga ttgtaagact attttaaaag cattgggacc agcggctaca 720
ctagaagaaa tgatgacagc atgtcagggg gtaggaggac ccggccataa ggcaagagtt 780
ttgttattca taatgatagt aggaggcttg gtaggtttta gaatagtttt tgctgtactt 840
tctgtagtga atagagttag gcagggatat tcaccattat cgtttcagac ccacctccca 900
atcccagggg gataa 915

<210> 49
 <211> 232
 <212> PRT
 <213> Human immunodeficiency virus type 1

<400> 49

Met Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His Gln Ala Ile
 1 5 10 15

Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu Lys Ala
 20 25 30

Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala
 35 40 45

Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
 50 55 60

Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu
 65 70 75 80

Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln
 85 90 95

Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu
 100 105 110

Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly
 115 120 125

Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
 130 135 140

Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu
 145 150 155 160

Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu
 165 170 175

Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val
 180 185 190

Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro
 195 200 205

Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
 210 215 220

10003035101

Pro Gly His Lys Ala Arg Val Leu
225 230

<210> 50
<211> 261
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 50

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Pro Ile
20 25 30

Val Gln Asn Ile Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg
35 40 45

Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu Lys Ala Phe Ser Pro
50 55 60

Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln
65 70 75 80

Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln Ala Ala Met
85 90 95

Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu Trp Asp Arg
100 105 110

Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln Met Arg Glu
115 120 125

Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln
130 135 140

Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr
145 150 155 160

Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser
165 170 175

Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg
180 185 190

10003035 110101

Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser
195 200 205

Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala
210 215 220

Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr
225 230 235 240

Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His
245 250 255

Lys Ala Arg Val Leu
260

<210> 51
<211> 286
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 51

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Pro Ile
20 25 30

Val Gln Asn Ile Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg
35 40 45

Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu Lys Ala Phe Ser Pro
50 55 60

Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln
65 70 75 80

Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln Ala Ala Met
85 90 95

Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Arg Glu Pro Arg
100 105 110

Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly
115 120 125

Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg
130 135 140

1003035-110101

Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr
145 150 155 160

Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr
165 170 175

Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu
180 185 190

Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro
195 200 205

Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu
210 215 220

Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His Lys Ala
225 230 235 240

Arg Val Leu Leu Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg
245 250 255

Ile Val Phe Ala Val Leu Ser Val Val Asn Arg Val Arg Gln Gly Tyr
260 265 270

Ser Pro Leu Ser Phe Gln Thr His Leu Pro Ile Pro Arg Gly
275 280 285

<210> 52
<211> 3839
<212> DNA
<213> Artificial sequence

<220>
<223> Modified Env/Tat

<400> 52
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ggcgttactc gacagaggag agcaagaaat ggagccagta gatcctagac tagagccctg 120
gaagcatcca ggaagtcagc ctaaaactgc ttgtaccaat tgctattgta aaaagtgttg 180
ctttcattgc caagtttgtt tcataacaaa agccttaggc atctcctatg gcaggaagaa 240
gcggagacag cgacgaagac ctctcaagg cagtcagact catcaagttt ctctatcaaa 300
gcagtaagta gtacatgtaa tgcaacctat acaaatagca atagtagcat tagtagtagc 360
aataataata gcaatagttg tgtgggtccat agtaatcata gaatatagga aaatattaag 420

acaaagaaaa	atagacaggt	taattgatag	actaatagaa	agagcagaag	acagtggcaa	480
tgagagtgaa	ggagaaatat	cagcacttgt	ggagatgggg	gtggagatgg	ggcaccatgc	540
tccttgggat	gttgatgata	tgtagtgtta	cagaaaaatt	gtgggtcaca	gtctattatg	600
gggtacctgt	gtggaaggaa	gcaaccacca	ctctattttg	tgcatacagat	gctaaagcat	660
atgatacaga	ggtacataat	gtttggggcca	cacatgcctg	tgtaccacaca	gaccccaacc	720
cacaagaagt	agtattggta	aatgtgacag	aaaattttta	catgtggaaa	aatgacatgg	780
tagaacagat	gcatgaggat	ataatcagtt	tatgggatca	aagcctaaag	ccatgtgtaa	840
aattaacccc	actctgtgtt	ggagctggta	gttgtaacac	ctcagtcatt	acacaggcct	900
gtccaaagggt	atcctttgag	ccaattccca	tacattattg	tgccccgggt	ggttttgcga	960
ttctaaaatg	taataataag	acgttcaatg	gaacaggacc	atgtacaaat	gtcagcacag	1020
tacaatgtac	acatggaatt	aggccagtag	tatcaactca	actgctgtta	aatggcagtc	1080
tggcagaaga	agaggtagta	attagatctg	ccaatttcac	agacaatgct	aaaaccataa	1140
tagtacagct	gaaccaatct	gtagaaatta	attgtacaag	acccaacaac	aatacaagaa	1200
aaagtatccg	tatccagaga	ggaccagggg	gagcatttgt	tacaatagga	aaaataggaa	1260
atatgagaca	agcacattgt	ctcgggtgta	ccagacctaa	caacaataca	agaaaaagtg	1320
tacgtatagg	accaggacaa	acattctatg	caacagggtga	tataataggg	gatataagac	1380
aagcacattg	ttgtacgaga	cccaacaata	atacaagaaa	aagtataagg	ataggaccag	1440
gacaagcatt	ctatgcaaca	ggagaaataa	taggagatat	aagacaagca	cattgtttgca	1500
caaggcccta	caacaatata	agacaaagga	cccccatagg	actagggcaa	gcactctata	1560
caacaagaag	aatagaagat	ataagaagag	cacattgttg	taccagaccc	tccaccaata	1620
caagaacaag	tatacgtata	ggaccaggac	aagtattcta	tagaacagga	gacataacag	1680
gagatataag	aaaagcatat	tgtggatcct	gtacaagacc	caacaacaat	acaagaaaaa	1740
gaatatcttt	aggaccagga	cgagtatttt	atacagcagg	agaaataata	ggagacatca	1800
gaaaggcaca	ttgttgtacc	agacctataa	acaatacaag	aaaaagtata	acttttgcac	1860
caggacaagc	gctctatgca	acaggtgaaa	taataggaga	tataagacaa	gcacattgtc	1920
tcgggtgtac	cagacctaac	aacaatacaa	gaaaaagtg	acgtatagga	ccaggacaaa	1980
cattctatgc	aacaggtgat	ataatagggg	atataagaca	agcacattgt	tgtacgagac	2040
ccaacaataa	tacaagaaaa	agtataagga	taggaccagg	acaagcattc	tatgcaacag	2100
gagaaataat	aggagatata	agacaagcac	attgttgcac	aaggccctac	aacaatataa	2160
gacaaaggac	ccccatagga	ctagggcaag	cactctatac	aacaagaaga	atagaagata	2220
taagaagagc	acattgttgt	accagaccct	ccaccaatac	aagaacaagt	atacgtatag	2280

gaccaggaca agtattctat agaacaggag acataacagg agatataaga aaagcatatt	2340
gtggatcctg tacaagaccc aacaacaata caagaaaaag aatatcttta ggaccaggac	2400
gagtatttta tacagcagga gaaataatag gagacatcag aaaggcacat tgttgtacca	2460
gacctaataa caatacaaga aaaagtataa cttttgcacc aggacaagcg ctctatgcaa	2520
caggtgaaat aataggagat ataagacaag cacattgtct cgggaacatt agtagagcaa	2580
aatggaataa cactttaaaa cagatagata gcaaattaag agaacaattt ggaaataata	2640
aaacaataat ctttaagcag tcctcaggag gggacccaga aattgtaacg cacagtttta	2700
attgtggagg ggaatttttc tactgtaatt caacacaact gtttaatagt acttggttta	2760
atagtacttg gagtactaaa gggtaaata aactgaagg aagtgcaca atcaccctcc	2820
catgcagaat aaaacaaatt ataaacatgt ggcaggaagt aggaaaagca atgtatgccc	2880
ctcccatcag tggacaaatt agatgttcat caaatattac agggctgcta ttaacaagag	2940
atggtggtaa tagcaacaat gagtccgaga tcttcagacc tggaggagga gatatgaggg	3000
acaattggag aagtgaatta tataaatata aagtagtaaa aattgaacca ttaggagtag	3060
caccaccaa ggcaaagaga agagtgggtgc agactagtgc agtgggaata ggagctttgt	3120
tccttggggtt cttgggagca gcaggaagca ctatgggcgc agcgtcaatg acgctgacgg	3180
tacaggccag acaattattg tctggtatag tgcagcagca gaacaatttg ctgagggcta	3240
ttgaggcgca acagcatctg ttgcaactca cagtctgggg catcaagcag ctccaggcaa	3300
gaatcctggc tgtggaaaga tacctaaagg atcaacagct cctggggatt tggggttgct	3360
ctggaaaact catttgcacc actgctgtgc cttggaatgc tagttggagt aataaatctc	3420
tggaaacagat ttggaataac atgacctgga tggagtggga cagagaaatt aacaattaca	3480
caagcttaat acactcctta attgaagaat cgcaaaacca gcaagaaaag aatgaacaag	3540
aattattgga attagataaa tgggcaagtt tgtggaattg gtttaacata acaaattggc	3600
tgtggtatat aaaattattc ataatgatag taggaggctt ggtaggttta agaatagttt	3660
ttgctgtact ttctgtagtg aatagagtta ggcagggata ttcaccatta tcgtttcaga	3720
cccacctccc aatcccaggg ggacccgaca ggcccgaagg aatagaagaa gaagggtggag	3780
agagagacag agacagatcc attcgattag tgaacggatc cttagcactt atctggtaa	3839

<210> 53
 <211> 1101
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Modified Env/Tat

<400> 53

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
20 25 30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
35 40 45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
50 55 60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65 70 75 80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
85 90 95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
100 105 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Gly
115 120 125

Ala Gly Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
130 135 140

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
145 150 155 160

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
165 170 175

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
180 185 190

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
195 200 205

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
210 215 220

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
225 230 235 240

10003035-10101

Lys Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile
245 250 255

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Leu Gly Cys Thr Arg
260 265 270

Pro Asn Asn Asn Thr Arg Lys Ser Val Arg Ile Gly Pro Gly Gln Thr
275 280 285

Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys
290 295 300

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Arg Ile Gly Pro
305 310 315 320

Gly Gln Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln
325 330 335

Ala His Cys Cys Thr Arg Pro Tyr Asn Asn Ile Arg Gln Arg Thr Pro
340 345 350

Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr Arg Arg Ile Glu Asp Ile
355 360 365

Arg Arg Ala His Cys Cys Thr Arg Pro Ser Thr Asn Thr Arg Thr Ser
370 375 380

Ile Arg Ile Gly Pro Gly Gln Val Phe Tyr Arg Thr Gly Asp Ile Thr
385 390 395 400

Gly Asp Ile Arg Lys Ala Tyr Cys Gly Ser Cys Thr Arg Pro Asn Asn
405 410 415

Asn Thr Arg Lys Arg Ile Ser Leu Gly Pro Gly Arg Val Phe Tyr Thr
420 425 430

Ala Gly Glu Ile Ile Gly Asp Ile Arg Lys Ala His Cys Cys Thr Arg
435 440 445

Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Phe Ala Pro Gly Gln Ala
450 455 460

Leu Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys
465 470 475 480

10003035-110101

Leu Gly Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Val Arg Ile
485 490 495

Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile
500 505 510

Arg Gln Ala His Cys Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser
515 520 525

Ile Arg Ile Gly Pro Gly Gln Ala Phe Tyr Ala Thr Gly Glu Ile Ile
530 535 540

Gly Asp Ile Arg Gln Ala His Cys Cys Thr Arg Pro Tyr Asn Asn Ile
545 550 555 560

Arg Gln Arg Thr Pro Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr Arg
565 570 575

Arg Ile Glu Asp Ile Arg Arg Ala His Cys Cys Thr Arg Pro Ser Thr
580 585 590

Asn Thr Arg Thr Ser Ile Arg Ile Gly Pro Gly Gln Val Phe Tyr Arg
595 600 605

Thr Gly Asp Ile Thr Gly Asp Ile Arg Lys Ala Tyr Cys Gly Ser Cys
610 615 620

Thr Arg Pro Asn Asn Asn Thr Arg Lys Arg Ile Ser Leu Gly Pro Gly
625 630 635 640

Arg Val Phe Tyr Thr Ala Gly Glu Ile Ile Gly Asp Ile Arg Lys Ala
645 650 655

His Cys Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Phe
660 665 670

Ala Pro Gly Gln Ala Leu Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
675 680 685

Arg Gln Ala His Cys Leu Gly Asn Ile Ser Arg Ala Lys Trp Asn Asn
690 695 700

Thr Leu Lys Gln Ile Asp Ser Lys Leu Arg Glu Gln Phe Gly Asn Asn
705 710 715 720

10003035-110101

Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val
 725 730 735
 Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr
 740 745 750
 Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp Ser Thr Lys Gly
 755 760 765
 Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu Pro Cys Arg Ile
 770 775 780
 Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala
 785 790 795 800
 Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu
 805 810 815
 Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu Ser Glu Ile Phe
 820 825 830
 Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr
 835 840 845
 Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys
 850 855 860
 Ala Lys Arg Arg Val Val Gln Thr Ser Ala Val Gly Ile Gly Ala Leu
 865 870 875 880
 Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser
 885 890 895
 Met Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln
 900 905 910
 Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu
 915 920 925
 Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala
 930 935 940
 Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys
 945 950 955 960
 Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp

10003035-110101

965

970

975

Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu
980 985 990

Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile
995 1000 1005

Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu
1010 1015 1020

Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asn Ile Thr
1025 1030 1035

Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile Val Gly Gly
1040 1045 1050

Leu Val Gly Leu Arg Ile Val Phe Ala Thr His Leu Pro Ile Pro
1055 1060 1065

Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu Gly Gly Glu
1070 1075 1080

Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser Leu Ala
1085 1090 1095

Leu Ile Trp
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<211> 4040

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<213> Artificial sequence

<220>

<223> Modified Env/Tat/Rev

<400> 54

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gaagcatcca ggaagtcagc ctaaaactgc ttgtaccaat tgctattgta aaaagtgttg 180

ctttcattgc caagtttggt tcataacaaa agccttaggc atctcctatg gcaggaagaa 240

gcggagacag cgacgaagac ctctcaagg cagtcagact catcaagttt ctctatcaaa 300

gcagtaagta gtacatgtaa tgcaacctat acaaatagca atagtagcat tagtagtagc 360

aataataata gcaatagttg tgtgggtccat agtaatcata gaatatagga aatatattaag 420

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gggtacctgt	gtggaaggaa	gcaaccacca	ctctattttg	tgcatcagat	gctaaagcat	660
atgatacaga	ggtacataat	gtttggggcca	cacatgcctg	tgtaccacca	gaccccaacc	720
cacaagaagt	agtattggta	aatgtgacag	aaaattttaa	catgtggaaa	aatgacatgg	780
tagaacagat	gcatgaggat	ataatcagtt	tatgggatca	aagcctaaag	ccatgtgtaa	840
aattaacccc	actctgtgtt	ggagctggta	gttgtaacac	ctcagtcatt	acacaggcct	900
gtccaaaggt	atcctttgag	ccaattccca	tacattattg	tgccccggct	ggttttgcca	960
ttctaaaatg	taataataag	acgttcaatg	gaacaggacc	atgtacaaat	gtcagcacag	1020
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tggcagaaga	agaggtagta	attagatctg	ccaatttcac	agacaatgct	aaaaccataa	1140
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cattctatgc	aacagggtgat	ataatagggg	atataagaca	agcacattgt	tgtacgagac	2040
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gagaaataat	aggagatata	agacaagcac	attgttgcac	aaggccctac	aacaatataa	2160
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acaattggag	aagtgaatta	tataaatata	aagtagtaaa	aattgaacca	ttaggagtag	3060
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cgaggattgt	ggaacttctg	ggacgcaggg	ggtgggaagc	cctcaaatat	tgggtggaatc	3960
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<210> 55
 <211> 1186
 <212> PRT
 <213> Artificial sequence

 <220>
 <223> Modified Env/Tat/Rev

 <400> 55

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
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Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
 20 25 30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
 35 40 45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
 50 55 60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
 65 70 75 80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
 85 90 95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
 100 105 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Gly
 115 120 125

Ala Gly Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
 130 135 140

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
 145 150 155 160

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
 165 170 175

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
 180 185 190

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile

10003035-110104

195					200					205					
Arg	Ser	Ala	Asn	Phe	Thr	Asp	Asn	Ala	Lys	Thr	Ile	Ile	Val	Gln	Leu
210						215					220				
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225					230					235					240
Lys	Ser	Ile	Arg	Ile	Gln	Arg	Gly	Pro	Gly	Arg	Ala	Phe	Val	Thr	Ile
				245					250					255	
Gly	Lys	Ile	Gly	Asn	Met	Arg	Gln	Ala	His	Cys	Leu	Gly	Cys	Thr	Arg
			260					265					270		
Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Val	Arg	Ile	Gly	Pro	Gly	Gln	Thr
			275				280					285			
Phe	Tyr	Ala	Thr	Gly	Asp	Ile	Ile	Gly	Asp	Ile	Arg	Gln	Ala	His	Cys
	290					295					300				
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	Arg	Ile	Gly	Pro
305					310					315					320
Gly	Gln	Ala	Phe	Tyr	Ala	Thr	Gly	Glu	Ile	Ile	Gly	Asp	Ile	Arg	Gln
				325					330					335	
Ala	His	Cys	Cys	Thr	Arg	Pro	Tyr	Asn	Asn	Ile	Arg	Gln	Arg	Thr	Pro
			340					345					350		
Ile	Gly	Leu	Gly	Gln	Ala	Leu	Tyr	Thr	Thr	Arg	Arg	Ile	Glu	Asp	Ile
		355					360					365			
Arg	Arg	Ala	His	Cys	Cys	Thr	Arg	Pro	Ser	Thr	Asn	Thr	Arg	Thr	Ser
	370					375					380				
Ile	Arg	Ile	Gly	Pro	Gly	Gln	Val	Phe	Tyr	Arg	Thr	Gly	Asp	Ile	Thr
385					390				395						400
Gly	Asp	Ile	Arg	Lys	Ala	Tyr	Cys	Gly	Ser	Cys	Thr	Arg	Pro	Asn	Asn
				405					410					415	
Asn	Thr	Arg	Lys	Arg	Ile	Ser	Leu	Gly	Pro	Gly	Arg	Val	Phe	Tyr	Thr
			420					425					430		
Ala	Gly	Glu	Ile	Ile	Gly	Asp	Ile	Arg	Lys	Ala	His	Cys	Cys	Thr	Arg
		435					440					445			

Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Phe Ala Pro Gly Gln Ala
450 455 460

Leu Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys
465 470 475 480

Leu Gly Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Val Arg Ile
485 490 495

Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile
500 505 510

Arg Gln Ala His Cys Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser
515 520 525

Ile Arg Ile Gly Pro Gly Gln Ala Phe Tyr Ala Thr Gly Glu Ile Ile
530 535 540

Gly Asp Ile Arg Gln Ala His Cys Cys Thr Arg Pro Tyr Asn Asn Ile
545 550 555 560

Arg Gln Arg Thr Pro Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr Arg
565 570 575

Arg Ile Glu Asp Ile Arg Arg Ala His Cys Cys Thr Arg Pro Ser Thr
580 585 590

Asn Thr Arg Thr Ser Ile Arg Ile Gly Pro Gly Gln Val Phe Tyr Arg
595 600 605

Thr Gly Asp Ile Thr Gly Asp Ile Arg Lys Ala Tyr Cys Gly Ser Cys
610 615 620

Thr Arg Pro Asn Asn Asn Thr Arg Lys Arg Ile Ser Leu Gly Pro Gly
625 630 635 640

Arg Val Phe Tyr Thr Ala Gly Glu Ile Ile Gly Asp Ile Arg Lys Ala
645 650 655

His Cys Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Phe
660 665 670

Ala Pro Gly Gln Ala Leu Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
675 680 685

10003035-110101

1160

1165

1170

Val Asn Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu
 1175 1180 1185

<210> 56
 <211> 507
 <212> DNA
 <213> Human immunodeficiency virus type 1

<400> 56
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 agaagagagc ttcaggtctg gggtagagac aacaactccc cctcagaagc aggagccgat 180
 agacaaggaa ctgtatcctt taacttcctt cagatcactc tttggcaacg acccctcgtc 240
 acaataaaga taggggggca actaaaggaa gctctattag atacaggagc agatgatata 300
 gtattagaag aaatgagttt gccaggaaga tggaaaccaa aaatgatagg ggggaattgga 360
 ggttttatca aagtaagaca gtatgatcag atactcatag aaatctgtgg acataaagct 420
 ataggtacag tattagtagg acctacacct gtcaacataa ttggaagaaa tctgttgact 480
 cagattgggt gcactttaaa tttttaa 507

<210> 57
 <211> 168
 <212> PRT
 <213> Human immunodeficiency virus type 1

<400> 57

Met Phe Phe Arg Glu Asp Leu Ala Phe Leu Gln Gly Lys Ala Arg Glu
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Phe Ser Ser Glu Gln Thr Arg Ala Asn Ser Pro Thr Ile Ser Ser Glu
 20 25 30

Gln Thr Arg Ala Asn Ser Pro Thr Arg Arg Glu Leu Gln Val Trp Gly
 35 40 45

Arg Asp Asn Asn Ser Pro Ser Glu Ala Gly Ala Asp Arg Gln Gly Thr
 50 55 60

Val Ser Phe Asn Phe Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val
 65 70 75 80

Thr Ile Lys Ile Gly Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly
 85 90 95

10003035-10101

Ala Asp Asp Thr Val Leu Glu Glu Met Ser Leu Pro Gly Arg Trp Lys
100 105 110

Pro Lys Met Ile Gly Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr
115 120 125

Asp Gln Ile Leu Ile Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val
130 135 140

Leu Val Gly Pro Thr Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr
145 150 155 160

Gln Ile Gly Cys Thr Leu Asn Phe
165

<210> 58
<211> 1800
<212> DNA
<213> Artificial sequence

<220>
<223> Gag-PI

<400> 58
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ttaaggccag ggggaaagaa aaaatataaa ttaaaacata tagtatgggc aagcagggag 120
ctagaacgat tcgcagttaa tcttgacctg ttagaaacat cagaaggctg tagacaaata 180
ctgggacagc tacaaccatc ccttcagaca ggatcagaag aacttagatc attatataat 240
acagtagcaa ccctctattg tgtgcatcaa aggatagaga taaaagacac caaggaagct 300
ttagacaaga tagaggaaga gcaaaacaaa agtaagaaaa aagcacagca agcagcagct 360
gacacaggac acagcagtca ggtcagccaa aattacccta tagtgcagaa catccagggg 420
caaagtgtac atcaggccat atcacctaga actttaaatg catgggtaaa agtagtagaa 480
gagaaggctt tcagcccaga agtaataccc atgttttcag cattatcaga aggagccacc 540
ccacaagatt taaacaccat gctaaacaca gtggggggac atcaagcagc catgcaaattg 600
ttaaaagaga ccatcaatga ggaagctgca gaatgggata gactacatcc agtgcattgca 660
gggcctattg caccaggcca gatgagagaa ccaaggggaa gtgacatagc aggaactact 720
agtacccttc aggaacaaat aggatggatg acaaataatc cacctatccc agtaggagaa 780
atttataaaa gatggataat cctgggatta aataaaatag taagaatgta tagccctacc 840
agcattctgg acataagaca aggacaaaaa gaacctttta gagactatgt agaccgggtc 900

10003035 "10101

tataaaactc taagagccga gcaagcttca caggaggtaa aaaattggat gacagaaacc 960
 ttgttggtcc aaaatgcgaa cccagattgt aagactatct taaaagcatt gggaccagcg 1020
 gctacactag aagaaatgat gacagcatgt caggagtag gaggaccgg ccataaggca 1080
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 ggcaatttta ggaaccaaag aaagatgggt aagtgtttca attgtggcaa agaagggcac 1200
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 gaagctctat tagatacagg agcagatgat acagtattag aagaaatgag tttgccagga 1620
 agatggaaac caaaaatgat agggggaatt ggaggtttta tcaaagtaag acagtatgat 1680
 cagatactca tagaaatctg tggacataaa gctataggta cagtattagt aggacctaca 1740
 cctgtcaaca taattggaag aaatctgttg actcagattg gttgcacttt aaatttttaa 1800

<210> 59
 <211> 599
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Gag-PI

<400> 59

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 1 5 10 15

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
 20 25 30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
 35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
 50 55 60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
 65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
85 90 95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
100 105 110

Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val
115 120 125

Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
130 135 140

Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
145 150 155 160

Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser
165 170 175

Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
180 185 190

Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu
195 200 205

Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala
210 215 220

Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
225 230 235 240

Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
245 250 255

Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
260 265 270

Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
275 280 285

Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
290 295 300

Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
305 310 315 320

Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala

FOOTNOTES - 110101

335

Gln Ile Leu Ile Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu
565 570 575

100303103

Val Gly Pro Thr Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln
 580 585 590

Ile Gly Cys Thr Leu Asn Phe
 595

<210> 60
 <211> 51
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer

<400> 60
 aaatcaaccg gaattgaatt ccctcgggtg taccagacct aacaacaata c 51

<210> 61
 <211> 42
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer

<400> 61
 attgttggtg ctcgtacaac aatgtgcttg tcttatatcc cc 42

<210> 62
 <211> 41
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer

<400> 62
 ggggatataa gacaagcaca ttgtacgaga cccaacaata c 41

<210> 63
 <211> 39
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer

<400> 63
 gttgtagggc ottgtgcaac aatgtgcttg tcttatatc 39

<210> 64
 <211> 39
 <212> DNA

FOOT "SEED" 100305-10101

<213> Artificial sequence

<220>

<223> PCR primer

<400> 64

gatataagac aagcacattg ttgcacaagg ccctacaac

39

<210> 65

<211> 36

<212> DNA

<213> Artificial sequence

<220>

<223> PCR primer

<400> 65

ggtggagggt ctggtacaac aatgtgctct tcttat

36

<210> 66

<211> 36

<212> DNA

<213> Artificial sequence

<220>

<223> PCR primer

<400> 66

ataagaagag cacattgttg taccagacc tccacc

36

<210> 67

<211> 47

<212> DNA

<213> Artificial sequence

<220>

<223> PCR primer

<400> 67

gtattgttgt tgggtcttgt acaacaatat gcttttctta tatctcc

47

<210> 68

<211> 47

<212> DNA

<213> Artificial sequence

<220>

<223> PCR primer

<400> 68

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47

<210> 69

<211> 39

<212> DNA

<213> Artificial sequence

10003035-110101

<220>
<223> PCR primer

<400> 69
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<210> 70
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer

<400> 70
gacatcagaa aggcacattg ttgtaccaga cctaataac 39

<210> 71
<211> 54
<212> DNA
<213> Artificial sequence

<220>
<223> PCR primer

<400> 71
aataaactag tctagacccc cgagtctaga acaatgtgct tgtcttatat ctcc 54

<210> 72
<211> 7
<212> DNA
<213> Artificial sequence

<220>
<223> MMLV SD site

<400> 72
aggtaag 7

<210> 73
<211> 9
<212> DNA
<213> Artificial sequence

<220>
<223> MMLV SA site

<400> 73
ctgctgcag 9

<210> 74
<211> 90
<212> DNA
<213> Artificial sequence



1.

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ctccttgggg tgttgatgat ctgtagtgct 90

<211> 129.

<213> Artificial sequence

<223> DNA encoding gp41 transmembrane domain

ttattcataa	tgatagtagg	aggcttggt	ggtttaagaa	tagtttttgc	tgtactttct	60
gtagtgaata	gagttaggca	gggatattca	ccattatcgt	ttcagaccca	cctcccaatc	120
ccgaggggga						129

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